



PCT09

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RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/09/806,232B

TIME: 14:16:43

Input Set : A:\1241.18 Sequence Listing.txt

Output Set: N:\CRF3\02062002\I806232B.raw

ENTERED

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3 <110> APPLICANT: Seiki Motoharu
5 <120> TITLE OF INVENTION: DNA CODING FOR NOVEL POLYPEPTIDE
7 <130> FILE REFERENCE: 1241.18
9 <140> CURRENT APPLICATION NUMBER: US 09/806,232B
C--> 10 <141> CURRENT FILING DATE: 2001-11-29
12 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05349
13 <151> PRIOR FILING DATE: 1999-09-29
15 <150> PRIOR APPLICATION NUMBER: JP10-276258
16 <151> PRIOR FILING DATE: 1998-09-29
18 <150> PRIOR APPLICATION NUMBER: JP10-291505
19 <151> PRIOR FILING DATE: 1998-09-29
21 <160> NUMBER OF SEQ ID NOS: 22
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 587
27 <212> TYPE: PRT
28 <213> ORGANISM: Mouse
30 <400> SEQUENCE: 1
31 Met Gly Arg Arg Pro Arg Gly Pro Gly Ser Pro Arg Gly Pro Gly Pro
32 1 5 10 15
34 Pro Arg Pro Gly Pro Gly Leu Pro Pro Leu Leu Val Leu Ala Leu
35 20 25 30
37 Ala Ala His Gly Gly Cys Ala Ala Pro Ala Pro Arg Ala Glu Asp Leu
38 35 40 45
40 Ser Leu Gly Val Glu Trp Leu Ser Arg Phe Gly Tyr Leu Pro Pro Ala
41 50 55 60
43 Asp Pro Ala Ser Gly Gln Leu Gln Thr Gln Glu Glu Leu Ser Lys Ala
44 65 70 75 80
46 Ile Thr Ala Met Gln Gln Phe Gly Gly Leu Glu Thr Thr Gly Ile Leu
47 85 90 95
49 Asp Glu Ala Thr Leu Ala Leu Met Lys Thr Pro Arg Cys Ser Leu Pro
50 100 105 110
52 Asp Leu Pro Pro Gly Ala Gln Ser Arg Arg Lys Arg Gln Thr Pro Pro
53 115 120 125
55 Pro Thr Lys Trp Ser Lys Arg Asn Leu Ser Trp Arg Val Arg Thr Phe
56 130 135 140
58 Pro Arg Asp Ser Pro Leu Gly Arg Asp Thr Val Arg Ala Leu Met Tyr
59 145 150 155 160
61 Tyr Ala Leu Lys Val Trp Ser Asp Ile Thr Pro Leu Asn Phe His Glu
62 165 170 175
64 Val Ala Gly Asn Ala Ala Asp Ile Gln Ile Asp Phe Ser Lys Ala Asp
65 180 185 190
67 His Asn Asp Gly Tyr Pro Phe Asp Gly Pro Gly Gly Thr Val Ala His

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68          195          200          205
70 Ala Phe Phe Pro Gly Asp His His Thr Ala Gly Asp Thr His Phe Asp
71          210          215          220
73 Asp Asp Glu Pro Trp Thr Phe Arg Ser Ser Asp Ala His Gly Met Asp
74 225          230          235          240
76 Leu Phe Ala Val Ala Val His Glu Phe Gly His Ala Ile Gly Leu Ser
77          245          250          255
79 His Val Ala Ala Pro Ser Ser Ile Met Gln Pro Tyr Tyr Gln Gly Pro
80          260          265          270
82 Val Gly Asp Pro Val Arg Tyr Gly Leu Pro Tyr Glu Asp Arg Val Arg
83          275          280          285
85 Val Trp Gln Leu Tyr Gly Val Arg Glu Ser Val Ser Pro Thr Ala Gln
86          290          295          300
88 Leu Asp Thr Pro Glu Pro Glu Glu Pro Pro Leu Leu Pro Glu Pro Pro
89 305          310          315          320
91 Asn Asn Arg Ser Ser Thr Pro Pro Gln Lys Asp Val Pro His Arg Cys
92          325          330          335
94 Thr Ala His Phe Asp Ala Val Ala Gln Ile Arg Gly Glu Ala Phe Phe
95          340          345          350
97 Phe Lys Gly Lys Tyr Phe Trp Arg Leu Thr Arg Asp Arg His Leu Val
98          355          360          365
100 Ser Leu Gln Pro Ala Gln Met His Arg Phe Trp Arg Gly Leu Pro Leu
101          370          375          380
103 His Leu Asp Ser Val Asp Ala Val Tyr Glu Arg Thr Ser Asp His Lys
104 385          390          395          400
106 Ile Val Phe Phe Lys Gly Asp Arg Tyr Trp Val Phe Lys Asp Asn Asn
107          405          410          415
109 Val Glu Glu Gly Tyr Pro Arg Pro Val Ser Asp Phe Ser Leu Pro Pro
110          420          425          430
112 Gly Gly Ile Asp Ala Val Phe Ser Trp Ala His Asn Asp Arg Thr Tyr
113          435          440          445
115 Phe Phe Lys Asp Gln Leu Tyr Trp Arg Tyr Asp Asp His Thr Arg Arg
116          450          455          460
118 Met Asp Pro Gly Tyr Pro Ala Gln Gly Pro Leu Trp Arg Gly Val Pro
119 465          470          475          480
121 Ser Met Leu Asp Asp Ala Met Arg Trp Ser Asp Gly Ala Ser Tyr Phe
122          485          490          495
124 Phe Arg Gly Gln Glu Tyr Trp Lys Val Leu Asp Gly Glu Leu Glu Ala
125          500          505          510
127 Ala Pro Gly Tyr Pro Gln Ser Thr Ala Arg Asp Trp Leu Val Cys Gly
128          515          520          525
130 Glu Pro Leu Ala Asp Ala Glu Asp Val Gly Pro Gly Pro Gln Gly Arg
131          530          535          540
133 Ser Gly Ala Gln Asp Gly Leu Ala Val Cys Ser Cys Thr Ser Asp Ala
134 545          550          555          560
136 His Arg Leu Ala Leu Pro Ser Leu Leu Leu Leu Thr Pro Leu Leu Trp
137          565          570          575
139 Gly Leu Trp Thr Ser Val Ser Ala Lys Ala Ser
140          580          585

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142 <210> SEQ ID NO: 2
143 <211> LENGTH: 606
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 2
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149 1 5 10 15
151 Gly Leu Ser Arg Leu Pro Leu Leu Pro Leu Pro Leu Leu Leu Leu
152 20 25 30
154 Ala Leu Gly Thr Arg Gly Gly Cys Ala Ala Pro Glu Pro Ala Arg Arg
155 35 40 45
157 Ala Glu Asp Leu Ser Leu Gly Val Glu Trp Leu Ser Arg Phe Gly Tyr
158 50 55 60
160 Leu Pro Pro Ala Asp Pro Thr Thr Gly Gln Leu Gln Thr Gln Glu Glu
161 65 70 75 80
163 Leu Ser Lys Ala Ile Thr Ala Met Gln Gln Phe Gly Gly Leu Glu Ala
164 85 90 95
166 Thr Gly Ile Leu Asp Glu Ala Thr Leu Ala Leu Met Lys Thr Pro Arg
167 100 105 110
169 Cys Ser Leu Pro Asp Leu Pro Val Leu Thr Gln Ala Arg Arg Arg Arg
170 115 120 125
172 Gln Ala Pro Ala Pro Thr Lys Trp Asn Lys Arg Asn Leu Ser Trp Arg
173 130 135 140
175 Val Arg Thr Phe Pro Arg Asp Ser Pro Leu Gly His Asp Thr Val Arg
176 145 150 155 160
178 Ala Leu Met Tyr Tyr Ala Leu Lys Val Trp Ser Asp Ile Ala Pro Leu
179 165 170 175
181 Asn Phe His Glu Val Ala Gly Ser Thr Ala Asp Ile Gln Ile Asp Phe
182 180 185 190
184 Ser Lys Ala Asp His Asn Asp Gly Tyr Pro Phe Asp Gly Pro Gly Gly
185 195 200 205
187 Thr Val Ala His Ala Phe Phe Pro Gly His His His Thr Ala Gly Asp
188 210 215 220
190 Thr His Phe Asp Asp Asp Glu Ala Trp Thr Phe Arg Ser Ser Asp Ala
191 225 230 235 240
193 His Gly Met Asp Leu Phe Ala Val Ala Val His Glu Phe Gly His Ala
194 245 250 255
196 Ile Gly Leu Ser His Val Ala Ala Ala His Ser Ile Met Arg Pro Tyr
197 260 265 270
199 Tyr Gln Gly Pro Val Gly Asp Pro Leu Arg Tyr Gly Leu Pro Tyr Glu
200 275 280 285
202 Asp Lys Val Arg Val Trp Gln Leu Tyr Gly Val Arg Glu Ser Val Ser
203 290 295 300
205 Pro Thr Ala Gln Pro Glu Glu Pro Pro Leu Leu Pro Glu Pro Pro Asp
206 305 310 315 320
208 Asn Arg Ser Ser Ala Pro Pro Arg Lys Asp Val Pro His Arg Cys Ser
209 325 330 335
211 Thr His Phe Asp Ala Val Ala Gln Ile Arg Gly Glu Ala Phe Phe Phe
212 340 345 350

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214 Lys Gly Lys Tyr Phe Trp Arg Leu Thr Arg Asp Arg His Leu Val Ser
215          355          360          365
217 Leu Gln Pro Ala Gln Met His Arg Phe Trp Arg Gly Leu Pro Leu His
218          370          375          380
220 Leu Asp Ser Val Asp Ala Val Tyr Glu Arg Thr Ser Asp His Lys Ile
221 385          390          395          400
223 Val Phe Phe Lys Gly Asp Arg Tyr Trp Val Phe Lys Asp Asn Asn Val
224          405          410          415
226 Glu Glu Gly Tyr Pro Arg Pro Val Ser Asp Phe Ser Leu Pro Pro Gly
227          420          425          430
229 Gly Ile Asp Ala Ala Phe Ser Trp Ala His Asn Asp Arg Thr Tyr Phe
230          435          440          445
232 Phe Lys Asp Gln Leu Tyr Trp Arg Tyr Asp Asp His Thr Arg His Met
233          450          455          460
235 Asp Pro Gly Tyr Pro Ala Gln Ser Pro Leu Trp Arg Gly Val Pro Ser
236 465          470          475          480
238 Thr Leu Asp Asp Ala Met Arg Trp Ser Asp Gly Ala Ser Tyr Phe Phe
239          485          490          495
241 Arg Gly Gln Glu Tyr Trp Lys Val Leu Asp Gly Glu Leu Glu Val Ala
242          500          505          510
244 Pro Gly Tyr Pro Gln Ser Thr Ala Arg Asp Trp Leu Val Cys Gly Asp
245          515          520          525
247 Ser Gln Ala Asp Gly Ser Val Ala Ala Gly Val Asp Ala Ala Glu Gly
248          530          535          540
250 Pro Arg Ala Pro Pro Gly Gln His Asp Gln Ser Arg Ser Glu Asp Gly
251 545          550          555          560
253 Tyr Glu Val Cys Ser Cys Thr Ser Gly Ala Ser Ser Pro Pro Gly Ala
254          565          570          575
256 Pro Gly Pro Leu Val Ala Ala Thr Met Leu Leu Leu Leu Pro Pro Leu
257          580          585          590
259 Ser Pro Gly Ala Leu Trp Thr Ala Ala Gln Ala Leu Thr Leu
260          595          600          605
262 <210> SEQ ID NO: 3
263 <211> LENGTH: 3517
264 <212> TYPE: DNA
265 <213> ORGANISM: Mouse
267 <220> FEATURE:
268 <221> NAME/KEY: CDS
269 <222> LOCATION: (86)..(1846)
271 <400> SEQUENCE: 3
272 ggcaacgaggg cgcggagccg agcgaaggcgc ggagctggct gctggcgggt gcggggaccc 60
274 tcgccaccccg acctgggaga gcggg atg gga cgc cgc ccg cgg gga cct ggg 112
275          Met Gly Arg Arg Pro Arg Gly Pro Gly
276          1          5
278 tcc ccc cgg gga cct ggc cct cca cgc ccc ggg ccg ggg ctg cca cca 160
279 Ser Pro Arg Gly Pro Gly Pro Pro Arg Pro Gly Pro Gly Leu Pro Pro
280 10          15          20          25
282 ctg ctg ctt gta ctg gcg ctg gcg gcc cat ggg ggc tgc gca gcg ccc 208
283 Leu Leu Leu Val Leu Ala Leu Ala Ala His Gly Gly Cys Ala Ala Pro

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284		30		35		40	
286	gcg ccc cgc gcg gag gac ctc agc ctc ggg gtg gag tgg cta agc agg						256
287	Ala Pro Arg Ala Glu Asp Leu Ser Leu Gly Val Glu Trp Leu Ser Arg						
288		45		50		55	
290	ttt ggc tac ctg ccg cct gca gat ccg gca tca ggg cag cta cag acc						304
291	Phe Gly Tyr Leu Pro Pro Ala Asp Pro Ala Ser Gly Gln Leu Gln Thr						
292		60		65		70	
294	cag gag gaa ctg tcc aaa gcg att act gcc atg cag cag ttt ggt ggt						352
295	Gln Glu Glu Leu Ser Lys Ala Ile Thr Ala Met Gln Gln Phe Gly Gly						
296		75		80		85	
298	ctg gag acc act ggc atc cta gat gag gcc act ctg gcc ctg atg aaa						400
299	Leu Glu Thr Thr Gly Ile Leu Asp Glu Ala Thr Leu Ala Leu Met Lys						
300	90		95		100		105
302	acc cct cga tgc tcc ctt ccg gac ctg ccc cct ggg gcc caa tcg aga						448
303	Thr Pro Arg Cys Ser Leu Pro Asp Leu Pro Pro Gly Ala Gln Ser Arg						
304		110		115		120	
306	agg aag cgg cag act cca ccc cca acc aaa tgg agc aag agg aac ctt						496
307	Arg Lys Arg Gln Thr Pro Pro Pro Thr Lys Trp Ser Lys Arg Asn Leu						
308		125		130		135	
310	tct tgg agg gtc cgg aca ttc cca cgg gac tca ccc ctg ggc cgg gat						544
311	Ser Trp Arg Val Arg Thr Phe Pro Arg Asp Ser Pro Leu Gly Arg Asp						
312		140		145		150	
314	act gtg cgt gca ctc atg tac tac gcc ctc aaa gtc tgg agt gac atc						592
315	Thr Val Arg Ala Leu Met Tyr Tyr Ala Leu Lys Val Trp Ser Asp Ile						
316		155		160		165	
318	aca ccc ttg aac ttc cac gag gta gcg ggc aac gcg gcg gac atc cag						640
319	Thr Pro Leu Asn Phe His Glu Val Ala Gly Asn Ala Ala Asp Ile Gln						
320	170		175		180		185
322	atc gac ttc tcc aag gcc gac cac aat gac ggc tac ccc ttc gat ggc						688
323	Ile Asp Phe Ser Lys Ala Asp His Asn Asp Gly Tyr Pro Phe Asp Gly						
324		190		195		200	
326	cct ggt ggc acg gtg gcc cac gca ttc ttc cct ggt gac cac cac acg						736
327	Pro Gly Gly Thr Val Ala His Ala Phe Phe Pro Gly Asp His His Thr						
328		205		210		215	
330	gca ggg gac acc cac ttt gat gac gat gag cca tgg acc ttc cgt tcc						784
331	Ala Gly Asp Thr His Phe Asp Asp Asp Glu Pro Trp Thr Phe Arg Ser						
332		220		225		230	
334	tca gat gcc cac ggg atg gac ctg ttt gca gtg gcc gtc cat gag ttt						832
335	Ser Asp Ala His Gly Met Asp Leu Phe Ala Val Ala Val His Glu Phe						
336		235		240		245	
338	ggt cat gcc att ggt ctg agc cat gtt gcc gcc cca agc tcc atc atg						880
339	Gly His Ala Ile Gly Leu Ser His Val Ala Ala Pro Ser Ser Ile Met						
340	250		255		260		265
342	caa ccg tac tac cag ggc ccc gtg ggt gac ccc gta cgc tat gga ctt						928
343	Gln Pro Tyr Tyr Gln Gly Pro Val Gly Asp Pro Val Arg Tyr Gly Leu						
344		270		275		280	
346	ccc tat gag gac agg gtg cgt gtc tgg cag ttg tac ggt gtg cgg gaa						976
347	Pro Tyr Glu Asp Arg Val Arg Val Trp Gln Leu Tyr Gly Val Arg Glu						
348		285		290		295	

VERIFICATION SUMMARY

DATE: 02/06/2002

PATENT APPLICATION: US/09/806,232B

TIME: 14:16:44

Input Set : A:\1241.18 Sequence Listing.txt

Output Set: N:\CRF3\02062002\I806232B.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date